



SEQUENCE LISTING

<110> RASMUSSEN, Peter Birk
JENSEN, Martin Roland
NIELSEN, Klaus Gregorius
KOEFOED, Peter
DEGAN, Florence Dal

<120> Novel Method For Down-Regulation Of Amyloid

<130> 674542-2017

<140> 10/783,317
<141> 2004-02-20

<150> PCT/DK02/00547
<151> 2002-08-20

<150> 60/373,027
<151> 2002-04-16

<150> PA 2002 00558
<151> 2002-04-16

<150> 60/337,543
<151> 2001-10-22

<150> PA 2001 01231
<151> 2001-08-20

<160> 17

<170> PatentIn Ver. 3.1

<210> 1
<211> 2313
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(2313)

<220>
<221> misc_feature
<222> (2098)..(2169)
<223> nucleotides encoding transmembrane region

<220>
<221> misc_feature
<222> (2014)..(2313)
<223> Nucleotides encoding C-100

<220>
<221> misc_feature
<222> (2016)..(2144)
<223> Abeta 42/43

<220>

<221> misc_feature

<222> (2014)..(2142)

<223> Abeta 42/43

<400> 1

atg	ctg	ccc	ggt	ttg	gca	ctg	ctc	ctg	ctg	gcc	gcc	tgg	acg	gct	cgg	48
Met	Leu	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Ala	Trp	Thr	Ala	Arg	
1				5					10					15		
gcg	ctg	gag	gta	ccc	act	gat	ggt	aat	gct	ggc	ctg	ctg	gct	gaa	ccc	96
Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro	
			20					25					30			
cag	att	gcc	atg	ttc	tgt	ggc	aga	ctg	aac	atg	cac	atg	aat	gtc	cag	144
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln	
		35					40					45				
aat	ggg	aag	tgg	gat	tca	gat	cca	tca	ggg	acc	aaa	acc	tgc	att	gat	192
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp	
	50					55					60					
acc	aag	gaa	ggc	atc	ctg	cag	tat	tgc	caa	gaa	gtc	tac	cct	gaa	ctg	240
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu	
	65				70					75					80	
cag	atc	acc	aat	gtg	gta	gaa	gcc	aac	caa	cca	gtg	acc	atc	cag	aac	288
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn	
				85					90					95		
tgg	tgc	aag	cgg	ggc	cgc	aag	cag	tgc	aag	acc	cat	ccc	cac	ttt	gtg	336
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val	
			100					105					110			
att	ccc	tac	cgc	tgc	tta	gtt	ggt	gag	ttt	gta	agt	gat	gcc	ctt	ctc	384
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu	
		115					120					125				
gtt	cct	gac	aag	tgc	aaa	ttc	tta	cac	cag	gag	agg	atg	gat	gtt	tgc	432
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys	
	130					135					140					
gaa	act	cat	ctt	cac	tgg	cac	acc	gtc	gcc	aaa	gag	aca	tgc	agt	gag	480
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu	
	145				150				155						160	
aag	agt	acc	aac	ttg	cat	gac	tac	ggc	atg	ttg	ctg	ccc	tgc	gga	att	528
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile	
				165					170					175		
gac	aag	ttc	cga	ggg	gta	gag	ttt	gtg	tgt	tgc	cca	ctg	gct	gaa	gaa	576
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu	
			180					185					190			
agt	gac	aat	gtg	gat	tct	gct	gat	gcg	gag	gag	gat	gac	tcg	gat	gtc	624
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	

195	200	205	
tgg tgg ggc gga gca gac aca gac tat gca gat ggg agt gaa gac aaa Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys 210 215 220			672
gta gta gaa gta gca gag gag gaa gaa gtg gct gag gtg gaa gaa gaa Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu 225 230 235 240			720
gaa gcc gat gat gac gag gac gat gag gat ggt gat gag gta gag gaa Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu 245 250 255			768
gag gct gag gaa ccc tac gaa gaa gcc aca gag aga acc acc agc att Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile 260 265 270			816
gcc acc acc acc acc acc acc aca gag tct gtg gaa gag gtg gtt cga Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg 275 280 285			864
gag gtg tgc tct gaa caa gcc gag acg ggg ccg tgc cga gca atg atc Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile 290 295 300			912
tcc cgc tgg tac ttt gat gtg act gaa ggg aag tgt gcc cca ttc ttt Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe 305 310 315 320			960
tac ggc gga tgt ggc ggc aac cgg aac aac ttt gac aca gaa gag tac Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr 325 330 335			1008
tgc atg gcc gtg tgt ggc agc gcc atg tcc caa agt tta ctc aag act Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr 340 345 350			1056
acc cag gaa cct ctt gcc cga gat cct gtt aaa ctt cct aca aca gca Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala 355 360 365			1104
gcc agt acc cct gat gcc gtt gac aag tat ctc gag aca cct ggg gat Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp 370 375 380			1152
gag aat gaa cat gcc cat ttc cag aaa gcc aaa gag agg ctt gag gcc Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala 385 390 395 400			1200
aag cac cga gag aga atg tcc cag gtc atg aga gaa tgg gaa gag gca Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala 405 410 415			1248
gaa cgt caa gca aag aac ttg cct aaa gct gat aag aag gca gtt atc Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile 420 425 430			1296

cag cat ttc cag gag aaa gtg gaa tct ttg gaa cag gaa gca gcc aac	1344
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn	
435 440 445	
gag aga cag cag ctg gtg gag aca cac atg gcc aga gtg gaa gcc atg	1392
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met	
450 455 460	
ctc aat gac cgc cgc cgc ctg gcc ctg gag aac tac atc acc gct ctg	1440
Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu	
465 470 475 480	
cag gct gtt cct cct cgg cct cgt cac gtg ttc aat atg cta aag aag	1488
Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys	
485 490 495	
tat gtc cgc gca gaa cag aag gac aga cag cac acc cta aag cat ttc	1536
Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe	
500 505 510	
gag cat gtg cgc atg gtg gat ccc aag aaa gcc gct cag atc cgg tcc	1584
Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser	
515 520 525	
cag gtt atg aca cac ctc cgt gtg att tat gag cgc atg aat cag tct	1632
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser	
530 535 540	
ctc tcc ctg ctc tac aac gtg cct gca gtg gcc gag gag att cag gat	1680
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp	
545 550 555 560	
gaa gtt gat gag ctg ctt cag aaa gag caa aac tat tca gat gac gtc	1728
Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val	
565 570 575	
ttg gcc aac atg att agt gaa cca agg atc agt tac gga aac gat gct	1776
Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala	
580 585 590	
ctc atg cca tct ttg acc gaa acg aaa acc acc gtg gag ctc ctt ccc	1824
Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro	
595 600 605	
gtg aat gga gag ttc agc ctg gac gat ctc cag ccg tgg cat tct ttt	1872
Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe	
610 615 620	
ggg gct gac tct gtg cca gcc aac aca gaa aac gaa gtt gag cct gtt	1920
Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val	
625 630 635 640	
gat gcc cgc cct gct gcc gac cga gga ctg acc act cga cca ggt tct	1968
Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser	
645 650 655	

ggg ttg aca aat atc aag acg gag gag atc tct gaa gtg aag atg gat	2016
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp	
660 665 670	

gca gaa ttc cga cat gac tca gga tat gaa gtt cat cat caa aaa ttg	2064
Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu	
675 680 685	

gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att gga	2112
Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly	
690 695 700	

ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg atc gtc atc acc ttg	2160
Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu	
705 710 715 720	

gtg atg ctg aag aag aaa cag tac aca tcc att cat cat ggt gtg gtg	2208
Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val	
725 730 735	

gag gtt gac gcc gct gtc acc cca gag gag cgc cac ctg tcc aag atg	2256
Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met	
740 745 750	

cag cag aac ggc tac gaa aat cca acc tac aag ttc ttt gag cag atg	2304
Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met	
755 760 765	

cag aac tag	2313
Gln Asn	
770	

<210> 2
 <211> 770
 <212> PRT
 <213> Homo sapiens

<400> 2	
Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg	
1 5 10 15	
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro	
20 25 30	
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln	
35 40 45	
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp	
50 55 60	
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu	
65 70 75 80	
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn	
85 90 95	

Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val			
			100					105					110					
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu			
		115					120					125						
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys			
		130				135					140							
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu			
145					150					155					160			
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile			
			165						170					175				
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu			
			180					185					190					
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val			
		195					200					205						
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys			
		210				215					220							
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu			
225					230					235					240			
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu			
				245				250						255				
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile			
			260					265					270					
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg			
		275					280					285						
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile			
	290					295				300								
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe			
305					310					315					320			
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr			
				325					330					335				
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr			
			340					345					350					
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala			
		355					360					365						
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp			
		370				375					380							
Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala			
385					390					395					400			

Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	
				405					410					415		
Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	
			420					425					430			
Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	
		435					440					445				
Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	
	450					455					460					
Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	
465					470					475					480	
Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	
				485					490					495		
Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	
		500						505					510			
Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	
	515						520					525				
Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln	Ser	
	530					535					540					
Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	Glu	Glu	Ile	Gln	Asp	
545					550					555					560	
Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	Tyr	Ser	Asp	Asp	Val	
			565					570						575		
Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	Tyr	Gly	Asn	Asp	Ala	
		580						585					590			
Leu	Met	Pro	Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr	Val	Glu	Leu	Leu	Pro	
	595						600					605				
Val	Asn	Gly	Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln	Pro	Trp	His	Ser	Phe	
	610					615					620					
Gly	Ala	Asp	Ser	Val	Pro	Ala	Asn	Thr	Glu	Asn	Glu	Val	Glu	Pro	Val	
625					630					635					640	
Asp	Ala	Arg	Pro	Ala	Ala	Asp	Arg	Gly	Leu	Thr	Thr	Arg	Pro	Gly	Ser	
			645						650					655		
Gly	Leu	Thr	Asn	Ile	Lys	Thr	Glu	Glu	Ile	Ser	Glu	Val	Lys	Met	Asp	
		660					665						670			
Ala	Glu	Phe	Arg	His	Asp	Ser	Gly	Tyr	Glu	Val	His	His	Gln	Lys	Leu	
	675						680					685				
Val	Phe	Phe	Ala	Glu	Asp	Val	Gly	Ser	Asn	Lys	Gly	Ala	Ile	Ile	Gly	
	690					695					700					

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 3
<211> 45
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(45)
<223> DNA encoding P2 epitope

<400> 3
cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 4
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 4
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 5
<211> 63
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(63)
<223> DNA encoding P30 epitope

<400> 5
ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

gct agc cac ctg gaa 63

Ala Ser His Leu Glu
20

<210> 6
<211> 21
<212> PRT
<213> Clostridium tetani

<400> 6
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu
20

<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#105

<400> 7
caactcagct tcctttcggg c 21

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#178

<400> 8
agatctcgat cccgcgaaat t 21

<210> 9
<211> 135
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#800

<400> 9
atggatgcag aattccgtca cgactccggt tacgaagttc accaccagaa actgggttttc 60
ttcgcagaag atgttggttc caacaaagggt gcaatcatcg gtctgatggt tggcgggtgtt 120
gttatcgcga cctag 135

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#801

<400> 10

gccggccatg gatgcagaat tccgtcacga c 31

<210> 11
<211> 39
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#802

<400> 11
gccggaagct tctaggtcgc gataacaaca ccgccaacc 39

<210> 12
<211> 84
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#806

<400> 12
ccggcaagct tctacagctc ggtgataccg atgaatttgg agttagcttt gatgtactgg 60
gtcgcgataa caacaccgcc aacc 84

<210> 13
<211> 101
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#807

<400> 13
gccggccatg gggtttcaaca acttcaccgt tagcttctgg ctgcgtgttc cgaaagttag 60
cgcgagccac ctggaagatg cagaattccg tcacgactcc g 101

<210> 14
<211> 172
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#809

<400> 14
gggccaagct tggatccggt cgcgataaca acaccgcca ccatcagacc gatgattgca 60
cctttgttgg aaccaacatc ttctgcgaag aaaaccagtt tctggtggtg aacttcgtaa 120
ccggagtcgt gacggaactc tgcattccagc tcggtgatac cgatgaattt gg 172

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#810

<400> 15
ctggaagatg cagagttccg tcacgactcc 30

<210> 16

<211> 35
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer ME#811

<400> 16
gcgccggatc cttcaacaac ttcaccgtta gcttc

35

<210> 17
<211> 13
<212> PRT
<213> Artificial Sequence
<220>
<223> Artificial HLA DR binding sequence

<400> 17
Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10